



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Rhode, Peter R.
Acevedo, Jorge
Burkhardt, Martin
Jiao, Jin-an
Wong, Hing C.
- (ii) TITLE OF THE INVENTION: SOLUBLE MHC COMPLEXES AND METHODS OF USE THEREOF
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
 - (B) STREET: 130 Water Street
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: usa
 - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/766,378
 - (B) FILING DATE: 19-JAN-2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/960,190
 - (B) FILING DATE: 29-OCT-1997
- (viii) ATTORNEY/AGENT INFORMATION:
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 - (B) REGISTRATION NUMBER: 33,860
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- (ix) TELECOMMUNICATION INFORMATION:
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 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCACCATG

8

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCCCCAAGC TTCCGGGCCA CCATGGCTCT GCAGATCCCC AGC

43

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCCCACTT AAGGTCCATTG GGCTGCTCAG CACC

34

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGGGGGCCA TGGCCGGAAA CTCCGAAAGG CATTTCG

37

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCGACTA GTCCACTCCA CAGTGATGGG GC

32

(2) INFORMATION FOR SEQ ID NO:6:
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGGGGGGCCA TGGCCGAAGA CGACATTGAG GCCGAC

36

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGACTAG TCCAGTGTTC CAGAACCGGC TC

32

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGGGGGATA TCTCTCAGGC TGTTCACGCT G

31

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGGGTTCG AAAAGTGTAC TTACGGGGGG CTGGAATCTC AGGTTC

46

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGGGGCTCG AGTATCAAAG AAGAACATGT GATCATC

37

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGGCGGGAT CCGTTCTCTG TAGTCTCTGG GAGAGG

36

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATAAGAGGA AGAAGAGTAC ATGCCGATGG AACCCGGGTG AG

42

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AATTCTTCAC CCGGGTTCCA TCGGCATGTA CTCTTCTTCC TCG

43

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCCCCGCTA GCGGAGGGGG CGGAAGCGGC GGAGGGGGGG ACACCCGACC ACGTTTCCTG	60
TGGCAGCCTA AGAGG	75

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCCCCGAAT TCCCCACTAG TCCATTCCAC TGTGAGAGGG CTTGTCAC	48
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(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGGGGGGGCCA TGGCCTACGA CAGAACCCCG TGGTG	35
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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGGGGACTA GTTCGCCGCT GCACTGTGAA GC	32
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(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGGGGTATG CATA CGACGA GAACCCCGTG GTG

33

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGGGGGACTA GTCCACTTCG AGGAACTGTT TCC

33

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCCTGGTC TCCTCTGTGA GTGG

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCACTCACAG AGGAGACCAG GAGG

24

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCCCCCACCG GTTACGACAA GCCCGTGGTG

30

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCCCCCATCG ATAAGTGTAC TTACGTGGGA GAGGGCTTGG AGCAT

45

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 6...1505
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG
Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val
1 5 10 15

50

GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT
Val Leu Met Val Leu Ser Ser Pro Arg Thr Leu Ser Ile Ser Gln Ala
20 25 30

98

GTT CAC GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA
Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg Ala Ser Gly
35 40 45

146

GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC
Gly Gly Ser Gly Gly Gly Asn Ser Glu Arg His Phe Val Val
50 55 60

194

CAG	TTC	AAG	GGC	GAG	TGC	TAC	TAC	ACC	AAC	GGG	ACG	CAG	CGC	ATA	CGG		242
Gln	Phe	Lys	Gly	Glu	Cys	Tyr	Tyr	Thr	Asn	Gly	Thr	Gln	Arg	Ile	Arg		
65						70					75						
CTC	GTG	ACC	AGA	TAC	ATC	TAC	AAC	CGG	GAG	GAG	TAC	GTG	CGC	TAC	GAC		290
Leu	Val	Thr	Arg	Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	Tyr	Val	Arg	Tyr	Asp		
80					85				90			95					
AGC	GAC	GTG	GGC	GAG	TAC	CGC	GCG	GTG	ACC	GAG	CTG	GGG	CGG	CCA	GAC		338
Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	Glu	Leu	Gly	Arg	Pro	Asp		
						100			105			110					
GCC	GAG	TAC	TGG	AAC	AGC	CAG	CCG	GAG	ATC	CTG	GAG	CGA	ACG	CGG	GCC		386
Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Pro	Glu	Ile	Leu	Glu	Arg	Thr	Arg	Ala		
						115			120			125					
GAG	GTG	GAC	ACG	GCG	TGC	AGA	CAC	AAC	TAC	GAG	GGG	CCG	GAG	ACC	AGC		434
Glu	Val	Asp	Thr	Ala	Cys	Arg	His	Asn	Tyr	Glu	Gly	Pro	Glu	Thr	Ser		
						130			135			140					
ACC	TCC	CTG	CGG	CGG	CTT	GAA	CAG	CCC	AAT	GTC	GCC	ATC	TCC	CTG	TCC		482
Thr	Ser	Leu	Arg	Arg	Leu	Glu	Gln	Pro	Asn	Val	Ala	Ile	Ser	Leu	Ser		
						145			150			155					
AGG	ACA	GAG	GCC	CTC	AAC	CAC	CAC	AAC	ACT	CTG	GTC	TGT	TCG	GTG	ACA		530
Arg	Thr	Glu	Ala	Leu	Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	Thr		
						160			165			170			175		
GAT	TTC	TAC	CCA	GCC	AAG	ATC	AAA	GTG	CGC	TGG	TTC	AGG	AAT	GGC	CAG		578
Asp	Phe	Tyr	Pro	Ala	Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	Gln		
						180			185			190					
GAG	GAG	ACA	GTG	GGG	GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT	GGG	GAC		626
Glu	Glu	Thr	Val	Gly	Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	Asp		
						195			200			205					
TGG	ACC	TTC	CAG	GTC	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CAT	CAG	GGA		674
Trp	Thr	Phe	Gln	Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	His	Gln	Gly		
						210			215			220					
GAG	GTC	TAC	ACC	TGC	CAT	GTG	GAG	CAT	CCC	AGC	CTG	AAG	AGC	CCC	ATC		722
Glu	Val	Tyr	Thr	Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	Ile		
						225			230			235					
ACT	GTG	GAG	TGG	ACT	AGT	GGT	GGC	GGC	AGC	GGC	GGT	GGT	GGT	TCC		770	
Thr	Val	Glu	Trp	Thr	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Ser		
						240			245			250			255		
GGT	GGC	GGC	GGT	TCT	GGC	GGT	GGC	GGT	TCC	TCG	AGT	GAA	GAC	GAC	ATT		818
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Ser	Ser	Ser	Glu	Asp	Asp	Ile
						260			265			270					
GAG	GCC	GAC	CAC	GTA	GGC	TTC	TAT	GGT	ACA	ACT	GTT	TAT	CAG	TCT	CCT		866
Glu	Ala	Asp	His	Val	Gly	Phe	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	Pro		
						275			280			285					

GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe 290 295 300	914
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT Tyr Val Asp Leu Asp Lys Lys Thr Val Trp Arg Leu Pro Glu Phe 305 310 315	962
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala 320 325 330 335	1010
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr 340 345 350	1058
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro 355 360 365	1106
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile 370 375 380	1154
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val 385 390 395	1202
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser 400 405 410 415	1250
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Ile 420 425 430	1298
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys 435 440 445	1346
CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr 450 455 460	1394
GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG Val Val Cys Ala Leu Gly Leu Ser Val Gly Leu Val Gly Ile Val Val 465 470 475	1442
GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA Gly Thr Ile Phe Ile Ile Gln Gly Leu Arg Ser Gly Gly Thr Ser Arg 480 485 490 495	1490
CAC CCA GGG CCT TTA TGA His Pro Gly Pro Leu 500	1508

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ala Leu Gln Ile Pro Ser Leu Leu Ser Ala Ala Val Val Val
1 5 10 15
Leu Met Val Leu Ser Ser Pro Arg Thr Leu Ser Ile Ser Gln Ala Val
20 25 30
His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg Ala Ser Gly Gly
35 40 45
Gly Gly Ser Gly Gly Gly Asn Ser Glu Arg His Phe Val Val Gln
50 55 60
Phe Lys Gly Glu Cys Tyr Tyr Asn Gly Thr Gln Arg Ile Arg Leu
65 70 75 80
Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu Tyr Val Arg Tyr Asp Ser
85 90 95
Asp Val Gly Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg Pro Asp Ala
100 105 110
Glu Tyr Trp Asn Ser Gln Pro Glu Ile Leu Glu Arg Thr Arg Ala Glu
115 120 125
Val Asp Thr Ala Cys Arg His Asn Tyr Glu Gly Pro Glu Thr Ser Thr
130 135 140
Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg
145 150 155 160
Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp
165 170 175
Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu
180 185 190
Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp
195 200 205
Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu
210 215 220
Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr
225 230 235 240
Val Glu Trp Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
245 250 255
Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Glu Asp Asp Ile Glu
260 265 270
Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly
275 280 285
Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr
290 295 300
Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly
305 310 315 320
Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala
325 330 335
Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro
340 345 350

Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val
355 360 365
Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe
370 375 380
Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr
385 390 395 400
Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe
405 410 415
His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr
420 425 430
Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His
435 440 445
Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val
450 455 460
Val Cys Ala Leu Gly Leu Ser Val Gly Leu Val Gly Ile Val Val Gly
465 470 475 480
Thr Ile Phe Ile Ile Gln Gly Leu Arg Ser Gly Gly Thr Ser Arg His
485 490 495
Pro Gly Pro Leu
500

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala Pro Tyr Ser Thr Leu Leu Pro Pro Glu Leu Ser Glu Thr Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Tyr Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro
1 5 10 15
Arg Thr Pro Pro
20

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Glu Glu Glu Glu Tyr Met Pro Met Glu Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TSGGGGSGGG GS~~GGGG~~S~~GGG~~ GSSS

24

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg
1 5 10 15
Thr Pro Pro

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Thr Thr Ala Pro Ser Ala
1 5 10 15
Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu
20 25 30
Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Thr Thr Ala Pro Arg Ala
1 5 10 15

Gln Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu
20 25 30
Lys Trp Lys Leu Gln Ala Leu Lys Lys Leu Ala Gln
35 40

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ASSGGGSGGG

10

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
1 5 10 15
Ser Tyr Ile Tyr Ala
20

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His
1 5 10 15
Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr
20 25 30
Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
35 40 45
Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln
50 55 60

Lys Asp Ile Leu Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg
65 70 75 80
His Asn Tyr Gly Val Val Glu Ser Phe Thr Val Gln Arg Arg
85 90

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro
1 5 10 15
Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe
20 25 30
His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe
35 40 45
Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala
50 55 60
Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Thr
65 70 75 80
Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro
85 90 95
Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys Phe Ile Asp Lys Phe
100 105 110
Thr Pro Pro Val Val Asn Val Thr Trp Leu Arg Asn Gly Lys Pro Val
115 120 125
Thr Thr Gly Val Ser Glu Thr Val Phe Leu Pro Arg Glu Asp His Leu
130 135 140
Phe Arg Lys Phe His Tyr Leu Pro Phe Leu Pro Ser Thr Glu Asp Val
145 150 155 160
Tyr Asp Cys Arg Val Glu His Trp Gly Leu Asp Glu Pro Leu Leu Lys
165 170 175
His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu Asn
180 185 190